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P11439

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Entry information

Entry name	TOXA_PSEAE
Primary accession number	P11439
Secondary accession number	Q9I4I7
Entered in Swiss-Prot in	Release 12, October 1989
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 46, February 2005
Name and origin of the protein	
Protein name	Exotoxin A [Precursor]
Synonyms	NAD-dependent ADP-ribosyltransferase EC 2.4.2.-
Gene name	Name: eta OrderedLocusNames: PA1148
From	Pseudomonas aeruginosa [TaxID: 287]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

References

- [1] NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 26-53.
 MEDLINE=84194063;PubMed=6201861 [NCBI, ExPASy, EBI, Israel, Japan]
 Gray G.L., Smith D.H., Baldrige J.S., Harkins R.N., Vasil M.L., Chen E.Y., Heyneker H.L.;
 "Cloning, nucleotide sequence, and expression in Escherichia coli of the exotoxin A structural gene
 of Pseudomonas aeruginosa.";
 Proc. Natl. Acad. Sci. U.S.A. 81:2645-2649(1984).
- [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 15692 / PAO1;
 DOI=10.1038/35023079;MEDLINE=20437337;PubMed=10984043 [NCBI, ExPASy, EBI, Israel,
 Japan]
 Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P., Hickey M.J., Brinkman
 F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrook-
 Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., , Olson M.V.;
 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
 Nature 406:959-964(2000).

[3] ACTIVE SITE.

MEDLINE=87250491;PubMed=2885323 [NCBI, ExPASy, EBI, Israel, Japan]

Carroll S.F., Collier R.J.;

"Active site of *Pseudomonas aeruginosa* exotoxin A. Glutamic acid 553 is photolabeled by NAD and shows functional homology with glutamic acid 148 of diphtheria toxin.";

J. Biol. Chem. 262:8707-8711(1987).

[4] DOMAINS.

MEDLINE=90375493;PubMed=2118903 [NCBI, ExPASy, EBI, Israel, Japan]

Chaudhary V.K., Jinno Y., Galo M.G., Fitzgerald D., Pastan I.;

"Mutagenesis of *Pseudomonas* exotoxin in identification of sequences responsible for the animal toxicity.";

J. Biol. Chem. 265:16306-16310(1990).

[5] DOMAINS.

MEDLINE=91006124;PubMed=2170123 [NCBI, ExPASy, EBI, Israel, Japan]

Bourdenet S., Vacheron M.-J., Guinand M., Michel G., Arminjon F.;

"Biochemical and immunochemical studies of proteolytic fragments of exotoxin A from *Pseudomonas aeruginosa*.";

Eur. J. Biochem. 192:379-385(1990).

[6] DISULFIDE BOND.

DOI=10.1021/bi991308+;MEDLINE=20068844;PubMed=10600112 [NCBI, ExPASy, EBI, Israel, Japan]

McKee M.L., FitzGerald D.J.;

"Reduction of furin-nicked *Pseudomonas* exotoxin A: an unfolding story.";

Biochemistry 38:16507-16513(1999).

[7] X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 424-638.

MEDLINE=96016159;PubMed=7568123 [NCBI, ExPASy, EBI, Israel, Japan]

Li M., Dyda F., Benhar I., Pastan I., Davies D.R.;

"The crystal structure of *Pseudomonas aeruginosa* exotoxin domain III with nicotinamide and AMP: conformational differences with the intact exotoxin.";

Proc. Natl. Acad. Sci. U.S.A. 92:9308-9312(1995).

[8] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 424-638.

DOI=10.1073/pnas.93.14.6902;MEDLINE=96293446;PubMed=8692916 [NCBI, ExPASy, EBI, Israel, Japan]

Li M., Dyda F., Benhar I., Pastan I., Davies D.R.;

"Crystal structure of the catalytic domain of *Pseudomonas* exotoxin A complexed with a nicotinamide adenine dinucleotide analog: implications for the activation process and for ADP ribosylation.";

Proc. Natl. Acad. Sci. U.S.A. 93:6902-6906(1996).

Comments

- **FUNCTION:** This toxin is a NAD-dependent ADP-ribosyltransferase. It catalyzes the transfer of the ADP ribosyl moiety of oxidized NAD onto elongation factor 2 (EF-2) thus arresting protein synthesis.
- **PTM:** The 8 cysteines participate in intrachain disulfide bonds.

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Cross-references

EMBL K01397; AAB59097.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

AE004544; AAG04537.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

PIR A30347; A30347.
C83503; C83503.

1AER; X-ray; A=425-634, B=425-625. [ExPASy / RCSB / EBI]
1DMA; X-ray; A/B=425-638. [ExPASy / RCSB / EBI]
PDB 1IKP; X-ray; A=26-638. [ExPASy / RCSB / EBI]
1IKQ; X-ray; A=26-638. [ExPASy / RCSB / EBI]
Detailed list of linked structures.

SWISS-3DIMAGE P11439.

CMR P11439; PA1148.

InterPro IPR008985; ConA_like_lec_gl.
Graphical view of domain structure.

ProDom [Domain structure / List of seq. sharing at least 1 domain]

HOBACGEN [Family / Alignment / Tree]

BLOCKS P11439.

ProtoNet P11439.

ProtoMap P11439.

PRESAGE P11439.

DIP P11439.

ModBase P11439.

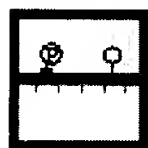
SMR P11439; 7B9AAD56A27C700A.

SWISS-2DPAGE Get region on 2D PAGE.

UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

3D-structure; Complete proteome; Direct protein sequencing; Glycosyltransferase; NAD; Signal; Toxin; Transferase.

Features

Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	25	25	
CHAIN	26	638	613	Exotoxin A.
DOMAIN	26	277	252	IA (required for target cell recognition).
DOMAIN	278	389	112	II (required for translocation in target cell cytoplasm).
DOMAIN	390	429	40	IB.
DOMAIN	430	638	209	III (required for ADP-ribosyl activity).
NP_BIND	465	481	17	NAD.
ACT_SITE	578	578		
DISULFID	290	312		
CONFLICT	4	4		T -> I (in Ref. 1).
CONFLICT	22	22		F -> S (in Ref. 1).
CONFLICT	204	204		A -> T (in Ref. 1). — 1A
CONFLICT	389	389		S -> N (in Ref. 1). — 11
CONFLICT	432	432		I -> V (in Ref. 1). — 13

denon
III

CONFLICT	540	540		G -> S (in Ref. 1).
STRAND	29	29	1	
HELIX	32	35	4	
STRAND	39	43	5	
TURN	45	46	2	
STRAND	49	54	6	
HELIX	57	60	4	
TURN	61	61	1	
STRAND	65	74	10	
TURN	76	79	4	
STRAND	81	85	5	
TURN	86	88	3	
STRAND	89	93	5	
STRAND	97	102	6	
STRAND	110	115	6	
STRAND	122	131	10	
TURN	132	133	2	
STRAND	137	145	9	
TURN	147	148	2	
STRAND	151	154	4	
STRAND	157	161	5	
HELIX	164	170	7	
TURN	171	172	2	
STRAND	173	180	8	
STRAND	189	201	13	
HELIX	213	216	4	
HELIX	218	223	6	
HELIX	225	227	3	
TURN	228	229	2	
HELIX	230	235	6	
HELIX	243	246	4	
TURN	247	247	1	
STRAND	249	255	7	
STRAND	262	262	1	
STRAND	270	273	4	
TURN	276	277	2	
HELIX	280	290	11	
TURN	291	291	1	
HELIX	294	298	5	
HELIX	307	311	5	
TURN	312	312	1	
HELIX	313	325	13	
TURN	326	327	2	
HELIX	330	332	3	
HELIX	333	342	10	
TURN	344	347	4	
HELIX	348	356	9	
HELIX	358	376	19	

TURN	377	378	2
TURN	380	381	2
HELIX	384	387	4
TURN	388	389	2
STRAND	392	396	5
HELIX	408	410	3
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STRAND	414	418	5
HELIX	422	424	3
TURN	436	437	2
TURN	440	441	2
HELIX	444	456	13
TURN	457	458	2
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HELIX	469	477	9
TURN	478	478	1
HELIX	489	491	3
STRAND	494	497	4
HELIX	500	504	5
TURN	505	506	2
STRAND	508	508	1
TURN	514	515	2
STRAND	520	520	1
STRAND	522	529	8
HELIX	530	535	6
STRAND	536	538	3
TURN	543	544	2
TURN	546	547	2
HELIX	548	556	9
TURN	557	557	1
STRAND	566	570	5
TURN	573	574	2
STRAND	577	581	5
HELIX	583	587	5
TURN	588	588	1
STRAND	590	593	4
TURN	600	601	2
TURN	603	604	2
HELIX	609	611	3
HELIX	614	617	4
TURN	618	619	2
STRAND	626	626	1

Sequence information

Length: **638 AA** [This is the length of the unprocessed precursor]

Molecular weight: **69284 Da** [This is the MW of the unprocessed precursor]

CRC64: **7B9AAD56A27C700A** [This is a checksum on the sequence]

10 20 30 40 50 60
MHLTPHWIPL VASLGLLAGG SFASAAEEAF DLWNECAKAC VLDLKDGVRS SRMSVDPAIA

70 80 90 100 110 120
DTNGQGVLHY SMVLEGGNDA LKLAI DNALS ITSDGLTIRL EGGVEPNKPV RYSYTRQARG

130 140 150 160 170 180
SWSLNWLVPI GHEKPSNIKV FIHEL NAGNQ LSHMSPIYTI EMGDELLAKL ARDATFFVRA

190 200 210 220 230 240
HESNEMQPTL AISHAGVSVV MAQAQPRREK RWSEWASGKV LCLLDPLDGV YNYLAQQRCN

250 260 270 280 290 300
LDDTWEGKIY RVLAGNPAKH DLDIKPTVIS HRLHFPEGGS LAALTAHQAC HLPLETFTRH

310 320 330 340 350 360
RQPRGWEQLE QCGYPVQRLV ALYLAARLSW NQVDQVIRNA LASPGSGGDL GEAIREQPEQ

370 380 390 400 410 420
ARLALTAAA ESERFVRQGT GNDEAGAASA DVVSLTCPVA AGECA GPADS GDALLERNYP

430 440 450 460 470 480
TGAEFLGDGG DISFSTRGTQ NWTVERLLQA HRQLEERGYV FVG YHGTFLE AAQSIVFGGV


490 500 510 520 530 540
RARSQDLDAI WRGFYIAGDP ALAYGYAQDQ EPDARGRIRN GALLRVYVPR SSLPGFYRTG

550 560 570 580 590 600
LTLAAPEAAG EVERLIGHPL PLRLDAITGP EEEGGRLETI LGWPLAERTV VIPSAIPTDP


610 620 630
RNVGGDL DPS SIPDKEQAIS ALPDYASQPG KPPREDLK

P11439 in FASTA format


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**BLAST**


BLAST submission on ExPASy/SIB or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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